



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

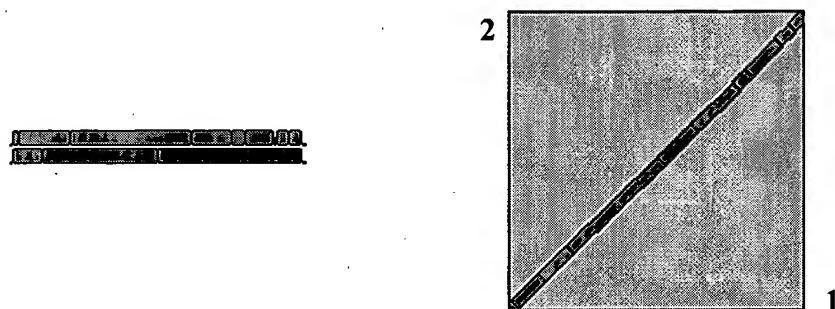
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ Align

Sequence 1 lcl|seq_1 Length 751 (1..751)

Sequence 2 lcl|seq_2 Length 771 (1..771)

Sema E
Sema D



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 708 bits (1827), Expect = 0.0

Identities = 339/757 (44%), Positives = 508/757 (66%), Gaps = 17/757 (2%)

Sequence alignment visualization showing a diagonal line of high similarity between two sequences.

```

Query: 4   RTICVLVGVFICSIC-VKGSSQPQARVYLTFDELRETKTSEYFSLSHHPLDYRILLMDED 62
          R +C+  GV + +      +      R+ L++ E+ E+      F+  +  Y  L+DE+
Sbjct: 6   RIVCLFWGVLLTARANYQNGKNNVPRCLKSYKEMLESNNVITFNGLANSSSYHTFLLDEE 65

Query: 63  QDRIYVGSKDHILSLNINNISQEALS VFWPASTIKVEECKMAGKDPHGCNPFVRVIQTF 122
          + R+YVG+KDHI S ++ NI ++      + WP S  + +ECK AGKD      C NF++V++ +
Sbjct: 66  RSRLYVGAKDHIFSFDLVNI-KDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAY 124

Query: 123 NRTHLYVCGSGAFSPVCTYLNRRGSRSEDQVFMID-SKCESGKGRCSFNPVNVTVSMINE 181
          N+THLY CG+GAF P+CTY+  G   ED +F ++ S  E+G+G+  ++P + T S++I+
Sbjct: 125 NQTHLYACGTGAFHPICTYIEIGHHPEDNIFKLENSHFENGRGKSPYDPKLLTASLLIDG 184

Query: 182 ELFGSMYIDFMGTDAAFRSLTKRNAVRTDQHNKWLSEPMFVDAHVIPDGTDPNDKQVY 241
          EL+SG   DFMG D AIFR+L   + +RT+QH+S+WL++P F+ AH+I +   +P D KQV
Sbjct: 185 ELYSGTAADFMGRDFAIFRTLGHHPHPIRTEQHDRWLNDPKFISAHLISESDNPEDDKVY 244

Query: 242 FFFKEKLTDNNRSTKQIHSMIARICPNDTGGRLSLVNKWTTFLLKARLVCSVTDEDGPETH 301
          FFF+E   D   S K  H+ I +IC ND GG RSLVNKWTTFLLKARL+CSV   +G +TH
Sbjct: 245 FFFRENAIDGEGHSGKATHARIGQICKNDFGGHRSVLVNKWTTFLLKARLICSVPGPNGIDTH 304

Query: 302 FDELEDVFLLETDPNRTTLVYGIFTTSSSVFKGSAVCVYHLSDIQTVFNGPFAHKEGPNH 361
          FDEL+DVFL+  +P+  +VYG+FTTSS++FKGSAVC+Y +SD++ VF GP+AH++GPN+
Sbjct: 305 FDELQDVFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPNY 364

Query: 362 QLISYQGRIPYPRPGTCPGAFTPNMRTTKEFPDDVVTFIRNHPLMYNSIYPIHKRPLIV 421
          Q + YQGR+PYPRPGTCP   F      +TK+ PDDV+TF R+HP MYN ++P++ RP+++
Sbjct: 365 QWVPYQGRVPYPRPGTCPSKTF-GGFDSTKDLPPDVITFARSHPAMYNPVFPMNNRPIVI 423
  
```

Query: 422 RIGTDYKYTKIAVDRVNAADGRYHVLFLGTDRGTVQKVVLPTNNSVS-GELILEEELEVF 480
+ +Y++T+I VDRV+A DG+Y V+F+GTD GTV KVV +P E++LEE+ VF
Sbjct: 424 KTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIKETWYDLEEVLLLEEMTVF 483

Query: 481 KNHAPITTMKISSKKQQLYVSSNEGVSQVSLHRCHYGTACADCCLARDPYCAWDGHSCS 540
+ I+ M++S+K+QQLY+ S GV+Q+ LHRC IYG ACA+CCLARDPYCAWDG +CS
Sbjct: 484 REPTAISAMELSTKQQLYIGSTAGVAQLPLHRCDIYGKACAECCCLARDPYCAWDGSACS 543

Query: 541 RFYPTGKRRSRRQDVRHGNPLTQCRGFNLKAY--RNAAEIVQYGVKNNTTFLECAPHKSPQ 598
R++PT KRR+RRQD+R+G+PLT C + + + E + YGV+N++TFLEC+PKS +
Sbjct: 544 RYFPTAKRRTRRQDIRNGDPLTHCSDLHHDNHHGHSPEERIIYGVENSSTFLECSPKSQ 603

Query: 599 ASIKWLLQ-KDKDRRKEVKLNERIIATSQGLLIRSVQGSQGLYHCIATENSFKQTIKI 657
A + W Q ++++R++E+++++ II T QGLL+RS+Q D G Y C A E+ F QT+ K+
Sbjct: 604 ALVYWQFQRRNEERKEEIRVDDHIIIRTDQGLLLRSLQKDSGNYLCHAVEHGFIQTLLKV 663

Query: 658 NFKVLDSEMAVVTDKWSPWTWA-----SSVRALPFHPKDIMGAFSHSEMQMINQYCK 710
+V+D+E + + K + S + +D M +H + ++++C+
Sbjct: 664 TLEVIDTEHLEELLHKDDGDGSKTKEMSNSMTPSQKVWYRDFMQLINHPNLNTMDEFCE 723

Query: 711 DT--RQQHQQGDSEQKMRGDYGLKALINSRKSRRNR 745
R + Q+ G+ K K L ++K RNRR
Sbjct: 724 QVWKRDRKQRRQRPGHTPGNSNKKWHLQENKKGRNR 760

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.321	0.135	0.413

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 4866

Number of Sequences: 0

Number of extensions: 399

Number of successful extensions: 8

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 751

length of database: 479,146,392

effective HSP length: 135

effective length of query: 616

effective length of database: 479,146,257

effective search space: 295154094312

effective search space used: 295154094312

T: 9

A: 40

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.8 bits)

S2: 79 (35.0 bits)